Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-109. Cancelled.

110. (Currently amended) A method for designing ~~an~~ a preferred oligonucleotide sequence having a selected duplex stability comprising:

a) providing an oligonucleotide sequence having ~~a sequence of~~ N bases and N-1 neighboring base pairs,

b) modifying the oligonucleotide sequence to provide modified oligonucleotide sequences wherein said modified oligonucleotide sequences ~~comprises~~ comprise at least one modified base selected from the group consisting of ~~a universal base,~~ unsubstituted pyrazolo[3,4-d]pyrimidines, ~~and~~ 3-substituted pyrazolo[3,4-d]pyrimidines, and 5-substituted pyrimidines;

~~b)~~ c) calculating the duplex ~~stability~~ stabilities of said modified oligonucleotide sequences using an algorithm applying a nearest-neighbor model for duplex formation thermodynamics for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases~~, optionally repeating steps a) b) to obtain a sequence having said selected duplex stability~~; ~~and~~

~~c) outputting the sequence to a user or a display~~

d) selecting a preferred oligonucleotide sequence from the modified oligonucleotide sequences having a selected duplex stability; and

e) creating an oligonucleotide comprising the preferred oligonucleotide sequence.

111. (Currently amended) A method for designing ~~an~~ a preferred oligonucleotide sequence having a selected duplex stability comprising:

a) providing an oligonucleotide sequence having ~~a sequence of~~ N bases and N-1 neighboring base pairs,

b) modifying the oligonucleotide sequence to provide modified oligonucleotide sequences wherein said modified oligonucleotide sequences ~~comprises~~ comprise at least one modified base selected from the group consisting of ~~a universal base,~~ unsubstituted pyrazolo[3,4-d]pyrimidines, ~~and~~ 3-substituted pyrazolo[3,4-d]pyrimidines, and 5-substituted pyrimidines[[;]], and a minor groove binder;

~~b)~~ c) calculating a melting temperature (T_m) of said modified oligonucleotide sequences using an algorithm applying nearest neighbor thermodynamic parameters for each of the N-1 neighboring base pairs, each nearest neighbor thermodynamic parameter defining a thermodynamic contribution of two corresponding neighboring bases~~, optionally repeating steps a) b) to obtain a sequence having said selected duplex stability~~; ~~and~~

~~c) outputting the sequence to a user or a display~~

d) selecting a preferred oligonucleotide sequence from the modified oligonucleotide sequences having the selected melting temperature; and

e) creating an oligonucleotide comprising the preferred oligonucleotide sequence.

112. (Previously presented) The method of any one of claims 110 or 111, wherein said oligonucleotide sequence is derived from a database source.

113. (Previously presented) The method of claim 112, wherein said database source is GENBANK.

114. (Currently amended) The method of any one of claims 110 or 111, wherein said at least one modified base is a member selected from the group consisting of a base attached to an amino acid, a polyamide nucleic acid (PNA), and a locked nucleic acid sugar.

115. (Previously presented) The method of claim 114, wherein said modified base is attached to PNA.

116. (Previously presented) The method of claim 114, wherein said modified base is attached to a locked nucleic acid sugar.

117. (Previously presented) The method of any one of claims 110 or 111, wherein said

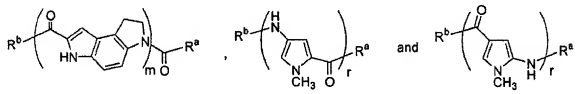
oligonucleotide has an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.

118. (Currently amended) The method of any one of claims 110 or 111, wherein said at least one modified base is a member selected from the group consisting of ~~a universal base,~~ PPA, PPG, PPPA, PPPG, PU, PC, HOPU, HOBuU, HOBuC, $(NH_2)_2$PPPA, $(NH_2)_2$PPPAOH, $(NH_2)_2$BuPPAOH, $(NH_2)_2$PPAI, and HOBuPPG.

119. (Currently amended) The method of claim 110, wherein said oligonucleotide has attached to it one or more members selected from the group consisting of a minor groove binder, a fluorophore, and a quencher.

120. (Currently amended) The method of claim 119, wherein said oligonucleotide ~~sequence~~ has a minor groove binder attached thereto.

121. (Currently amended) The method of claim 111 or 120, wherein said minor groove binder has a formula selected from the group consisting of:



wherein

the subscript m is an integer of from 2 to 5;

the subscript r is an integer of from 2 to 10; and

each R^a and R^b is independently a linking group to said modified oligonucleotide, H, OR^c, NR^cR^d, $COOR^c$, ~~or and~~ $--CONR^cR^d$ wherein each R^c and R^d is selected from the group consisting of H, $(C_1$-$C_{12})$heteroalkyl, $(C_2$-$C_{12})$heteroalkenyl, $(C_2$-$C_{12})$heteroalkynyl, $(C_1$-$C_{12})$alkyl, $(C_2$-$C_{12})$alkenyl, $(C_2$-$C_{12})$alkynyl, aryl$(C_1$-$C_{12})$alkyl, and aryl.

122. (Previously presented) The method of claim 120, wherein said minor groove binder is attached to the oligonucleotide via a quencher molecule.

123. (Previously presented) The method of any one of claims 110 or 111, wherein said algorithm predicts the melting temperature (T_m) of said oligonucleotide with an accuracy of about +/- 2° C.

124. (Currently amended) The method of any one of claims 110 or 111, wherein said method is applied to establish appropriate conditions for hybridization, renaturation, mapping variations of base compositions of sequences, or determination of sequence complexity and divergence.

125. (Previously presented) The method of any one of claims 110 or 111, wherein said oligonucleotide is a capture probe in an array.

126. (Currently amended) The method of claim 115, wherein said oligonucleotide has an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.

127. (Previously presented) The method of claim 116, wherein said oligonucleotide has an enhanced ability of mismatch discrimination, in comparison to unmodified nucleotides.

128. (New) The method of claim 110, wherein the oligonucleotide sequence comprises a universal base and wherein the modified oligonucleotide sequences comprise the universal base and at least one modified base selected from the group consisting of unsubstituted pyrazolo[3,4-d]pyrimidines, 3-substituted pyrazolo[3,4-d]pyrimidines, and 5-substituted pyrimidines.

129. (New) The method of claim 111, wherein the oligonucleotide sequence comprises a universal base and wherein the modified oligonucleotide sequences comprise the universal base and at least one modified base selected from the group consisting of unsubstituted pyrazolo[3,4-d]pyrimidines, 3-substituted pyrazolo[3,4-d]pyrimidines, and 5-substituted pyrimidines.